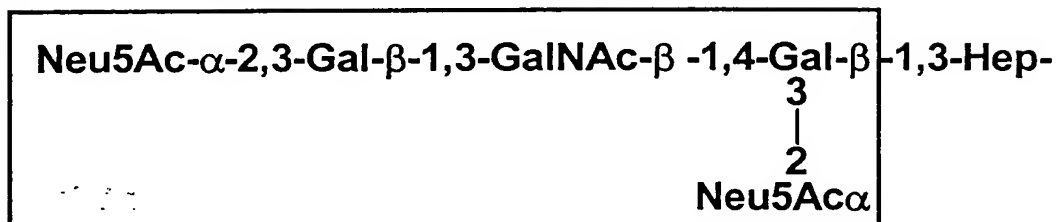
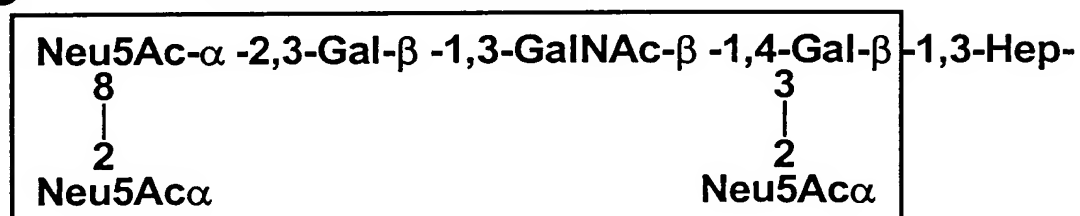


— 2 —

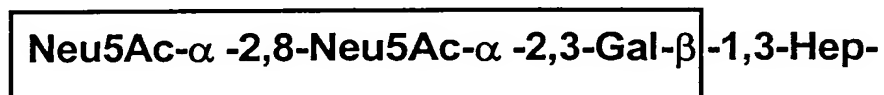
## O:19 serostrain



## O:19 strain OH4384



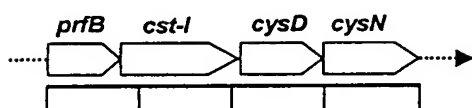
## O:19 strain OH4382



**Figure 2**

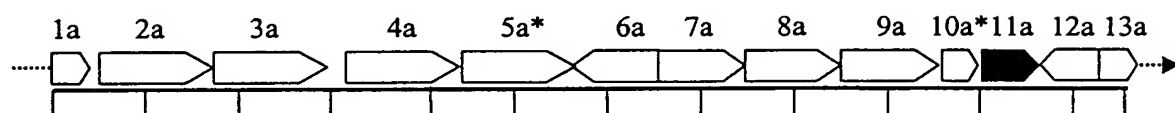
**A**

OH4384 *cst-I* locus (3.92 kb)



**B**

OH4382/OH4384 LOS biosynthesis locus (11.47 kb)



NCTC 11168 LOS biosynthesis locus (13.48 kb)

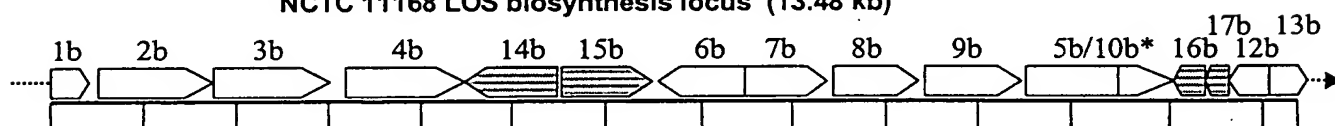


Figure 3

OH4384	-----MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDKYYLGKKC	45
O:19	-----MKKVIIAGNGPSLKEIDYSRLPNDFDVFRCNQFYFEDKYYLGKKC	45
Cst-I	MTRTRMENELIVSKNMQNI IAGNGPSLKNINYKRLPREYDVFRCNQFYFEDKYYLGKKI	60
11168	-----MSMNINALVCGNGPSLKNIDYKRLPKQFDVFRCNQFYFEDRYFVGKDV	48
Hi_ORF	----- ^ ^ ^ ^ ^   ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^	
OH4384	KAVFYNPILFFEQYYTLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPPDAHLG	105
O:19	KAVFYTPNFFFEQYYTLKHLIQNQEYETELIMCSNYNQAHLENENFVKTFYDYFPPDAHLG	105
Cst-I	KAVFFNPGVFLQQYHTAKQLILKNEYEIKNIFCSTFNLPFIESNDFLHQFYNFPPDAKLG	120
11168	KYVFFNPVFVFEQYYTSKKLIQNEEYNIENIVCSTINLEYIDGQFVDNFELYFSDAFLG	108
Hi_ORF	-----MQLIKNNEYEYADIILSSFVNLGDSELKKIKNVQKLLTQVDIG ^	43
OH4384	YDFFKQLKDFNAYFKFHEIYFNQRITSGVYMCVAIAIALGYKEIYLSGIDFYQN-GSSYAF	164
O:19	YDFFKQLKEFNAYFKFHEIYFNQRITSGVYMCVAIAIALGYKEIYLSGIDFYQN-GSSYAF	164
Cst-I	YEVLENLKEFYAYIKYNEIYFNKRITSGVYMCVAIAIALGYKTIYLCGIDFYEG-DVIYPP	179
11168	HEIIKKLKDFPAYIKYNEIYFNQRITSGVYMCATAVALGYKSIYISGIDFYQDTNNLYAF	168
Hi_ORF	HYILNKLPADFAYLQYNELYENKRITSGVYMCVATVMGYKDLYLTGIDFYQEKGNPYAF * ^ * * * ^ * ^ * ^ * ^ * ^ * ^ * ^ * ^ * ^ * ^ *	103
OH4384	DTKQKNLLKLAPNFKNDNSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELA	224
O:19	DTKQENLLKLAPDFKNDRSHYIGHSKNTDIKALEFLEKTYKIKLYCLCPNSLLANFIELA	224
Cst-I	EAMSTNIKTIFPGIK-DFKPSNCHSKEYDIEALKLLKSIYKVNIYALCDDSI LANHFPLS	238
11168	DNNKKNLLNKCTGFKNQKFKFINHSMACDLQALDYLKRYDVNIYSLNSD---EYFKLA	224
Hi_ORF	HHQKENI IKLLPSFSQNKSQSDIHSMEYDLNLYFLQKHVGVNIYICISPE SPLCNFYFPLS *           ^ ^ ^           * *   * * *   * ^ *           * ^ ^ ^   *	163
OH4384	PNLN-SNFIIQEK-NNYTKDILIPSSSEAYGKFSKN-----INFKKIK-IKENIYYK	272
O:19	PNLN-SNFIIQEK-NNYTKDILIPSSSEAYGKFSKN-----INFKKIK-IKENVYYK	272
Cst-I	ININ-NNFTLENKHNSINDILLTDNTPGVSFYKNQLKADNKIMLNFYNILHSDNLIK	297
11168	PDIG-SDFVLSKKPKKYINDILIPDKYAQERYYGK-----KSR-LKENLHYK	269
Hi_ORF	PLNNPITFILEEK-KNYTQDILIPPKFVYKKIGIYS-----KPR-IYQNLIFR ^ ^   *           *   ^ ^   * * * ^ ^                                   ^   ^   *	209
OH4384	LIKDLLRLPSDIKHYFKGK-----	291
O:19	LIKDLLRLPSDIKHYFKGK-----	291
Cst-I	LNKEIAVLKKQTTORAKARIQNHL	322
11168	LIKDLIRLPSDIKHYLKEKYANKNR	294
Hi_ORF	LIWDILRLPNDIKHALKSRKWD--- * ^ ^ ^           ^ * ^ ^ ^ ^           *	231

Figure 4

